to detect the normal and Scurfy PCR products, using the oligonucleotides below (the site of the 2 bp insertion is shown in bold):

Normal: ATGCAGCAAGAGCTCTTGTCCATTGAGG (SEQ ID NO: 11)
DMO7439

B9 cont

Scurfy: GCAGCAAGAGCTC**TT**TTGTCCATTGAGG (SEQ ID NO: 12)
DMO6919

Please replace the paragraph beginning at page 40, line 19, with the following rewritten paragraph:

The unique features of the *FKH*^{sf} gene sequence may be used to identify other novel genes (and proteins) which fall into the same sub-class of forkhead-containing molecules. The FKH^{sf} protein is unique in its having a single zinc finger domain amino-terminal to the forkhead domain as well as in the extreme carboxy-terminal position of the forkhead domain. A degenerate PCR approach may be taken to isolate novel genes containing a zinc finger sequence upstream of a forkhead domain. By way of example, the following degenerate primers were synthesized (positions of degeneracy are indicated by parentheses, and "I" indicates the nucleoside inosine):

B10

Forward primer: CA(TC)GGIGA(GA)TG(CT)AA(GA)TGG (SEQ ID NO:13)
Reverse primer: (GA)AACCA(GA)TT(AG)TA(AGT)AT(CT)TC(GA)TT (SEQ ID NO: 14)

REMARKS

The enclosed electronic and paper copies of the Sequence Listing include no new matter that goes beyond the original application as filed, but are supplied as requested by the Examiner. Furthermore, the above amendments, which merely direct the insertion of the Sequence Listing and insertion of sequence identifiers, include no matter that goes beyond the original

application as filed. Applicants respectfully submit that the above-identified application is now in compliance with 37 C.F.R. §§ 1.821-1.825 and WIPO Standard ST. 25.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The first of the attached pages is captioned "Version with Markings to Show Changes Made."

Respectfully submitted,
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Application No. : 09/697,340
Docket No. : 240083.501D4

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at page 5, line 4, has been amended as follows:

Figure 1 depicts a nucleotide sequence of mouse *Fkh*^{sf} cDNA ~~(Seqeunce I.D. No. 1)~~ (SEQ ID NO:1) ; translation is predicted to initiate at position 259 and terminate at position 1546.

Paragraph beginning at page 5, line 7, has been amended as follows:

Figure 2 depicts the amino acid sequence of mouse Fkh^{sf} ~~(Sequence I.D. No. 2)~~ (SEQ ID NO: 2).

Paragraph beginning at page 5, line 9, has been amended as follows:

Figure 3 depicts a nucleotide sequence of 1735 bp corresponding to human *FKHsf* cDNA (~~Sequence I.D. No. 3~~ SEQ ID NO: 3; including a 1293 bp coding region); translation is predicted to initiate at position 55 and terminate at position 1348.

Paragraph beginning at page 5, line 12, has been amended as follows:

Figure 4 depicts the sequence of a 431 amino acid human FKH^{sf} protein ~~(Sequence I.D. No. 4)~~ (SEQ ID NO: 4).

Paragraph beginning at page 34, line 4, has been amended as follows:

A complementary DNA (cDNA) encoding the complete mouse Fkh^{sf} protein may be obtained by a reverse-transcriptase polymerase chain reaction (RT-PCR) procedure. More specifically, first-strand cDNA is generated by oligo dT priming 5 ug of total RNA from a suitable source (eg., mouse spleen) and extending with reverse transcriptase under standard conditions (eg., Gibco/BRL SuperScript kit). An aliquot of the first-strand cDNA is then subjected to 35 cycles of PCR (94°C for 30 sec, 63°C for 30 sec, 72°C for 2 min) in the presence of the forward and reverse primers (Forward primer: GCAGATCTCC TGACTCTGCC TTC; SEQ ID NO: 5); Reverse primer: GCAGATCTGA CAAGCTGTGT CTG; SEQ ID NO: 6) (0.2 mM final concentration), 60 mM Tris-HCl, 15 mM ammonium sulfate, 1.5 mM magnesium chloride, 0.2 mM each dNTP and 1 unit of Taq polymerase.

Paragraph beginning at page 34, line 18, has been amended as follows:

A human *FKH^{sf}* cDNA encoding the complete FKH^{sf} protein may be obtained by essentially the same procedure as described in Example 2. In particular, starting with total spleen RNA, and utilizing the following oligonucleotide primers (Forward primer: AGCCTGCCCT TGGACAAGGA C; SEQ ID NO:7; Reverse primer: GCAAGACAGT GGAAACCTCA C; SEQ ID NO: 8), and the same PCR conditions outlined above, except with a 60°C annealing temperature.

Paragraph beginning at page 35, line 11, has been amended as follows:

As an example, a 360 bp DNA fragment is amplified from 1st strand cDNA using the following oligos:

DMO5985 (forward): CTACCCACTGCTGGCAAATG (ntd. 825-844 of Figure. 1)
(SEQ ID NO: 9)

DMO6724 (reverse): GAAGGAACTATTGCCATGGCTTC (ntd 1221-1199)

(SEQ ID NO: 10)

Paragraph beginning at page 35, line 20, has been amended as follows:

The PCR products are run on an 1.8% agarose gel, transferred to nylon membrane and probed with end-labeled oligonucleotides that are complementary to the region corresponding to the site of the Scurfy-specific 2 bp insertion. Two separate hybridization reactions are performed to detect the normal and Scurfy PCR products, using the oligonucleotides below (the site of the 2 bp insertion is shown in bold):

Normal: ATGCAGCAAGAGCTCTTGTCCATTGAGG (SEQ ID NO: 11)
DMO7439

Scurfy: GCAGCAAGAGCTC**TT**TTGTCCATTGAGG (SEQ ID NO: 12)
DMO6919

Paragraph beginning at page 40, line 19, has been amended as follows:

The unique features of the *FKH*^{sf} gene sequence may be used to identify other novel genes (and proteins) which fall into the same sub-class of forkhead-containing molecules. The FKH^{sf} protein is unique in its having a single zinc finger domain amino-terminal to the forkhead domain as well as in the extreme carboxy-terminal position of the forkhead domain. A degenerate PCR approach may be taken to isolate novel genes containing a zinc finger sequence upstream of a forkhead domain. By way of example, the following degenerate primers were synthesized (positions of degeneracy are indicated by parentheses, and "I" indicates the nucleoside inosine):

Forward primer: CA(TC)GGIGA(GA)TG(CT)AA(GA)TGG (SEQ ID NO: 13)
Reverse primer: (GA)AACCA(GA)TT(AG)TA(AGT)AT(CT)TC(GA)TT (SEQ ID NO: 14)